## Amendments to the claims:

Claim 1 (Previously Presented): A method of modifying an antibiotic-producing strain of Streptomyces coelicolor to increase antibiotic production in said strain, the method comprising functionally deleting in said strain the scbA gene by introducing a deletion, stop codon or frameshift into the coding sequence of said gene, wherein before said introduction said scbA gene encodes a polypeptide having the amino acid sequence of SEQ ID NO: 17.

Claims 2-8 (Cancelled)

Claim 9 (Previously Presented): A modified strain of Streptomyces coelicolor, the modified strain having a functional deletion of the schA gene, said functional deletion being effected by introducing a deletion, stop codon or frameshift into the coding sequence of said gene, whereby production of at least one antibiotic in said modified strain is increased compared to a wild-type strain of Streptomyces coelicolor, wherein before said introduction said schA gene encodes a polypeptide having the amino acid sequence of SEQ ID NO: 17.

Claim 10 (Cancelled)

Claim 11 (Previously Presented): The method of claim 1, wherein the strain is S. coelicolor A3(2).

Claim 12 (Cancelled)

Claim 13 (Previously Presented): The strain of claim 9, which is a modified strain of S. coelicolor A3(2).

Claim 14 (Cancelled)

Claim 15 (Currently Amended): A method for identifying

Streptomyces species in which antibiotic production is increased by the functional deletion of the schA gene of S. coelicolor or a homolog thereof, said schA gene having a nucleotide sequence which:

- (a) is the complement of nucleotides 2142-1199 of SEQ ID NO: 19; and/or
- (b) encodes a polypeptide having the amino acid sequence of SEQ ID NO: 17; and said homologue having a nucleotide sequence which has at least 90% sequence homology to the complement of nucleotides

the method comprising functionally deleting the scbA gene of S. coelicolor or said homolog thereof in an antibiotic-producing strain of a Streptomyces species by introducing a deletion, stop codon or frameshift into the coding sequence of said gene, the effect of said deletion on increasing said antibiotic production in said antibiotic-producing strain being unknown, said species being other than S. virginiae and S. griseus, culturing said strain under conditions suitable for the production of antibiotic, and determining whether antibiotic production in said strain is increased.

Claims 16-22 (Cancelled)

2142-1199 of SEQ ID NO: 19;

Claim 23 (Previously Presented): The method of claim 15, wherein said sequence identity is at least 95%.